RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/584,482_
Source: _1FWP_
Date Processed by STIC: _7/7/06_

ENTERED

IFWP

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RAW SEQUENCE LISTING                          DATE: 07/07/2006
PATENT APPLICATION:  US/10/584,482           TIME: 14:52:51

        Input Set : A:\PTO.KD.txt
        Output Set: N:\CRF4\07072006\J584482.raw

     3 <110> APPLICANT: HAGIWARA, Masatoshi
     5 <120> TITLE OF INVENTION: Method for controlling SR protein
phosphorylation, and antiviral agents
     6         whose active ingredients comprise agents that control SR protein
activity
     8 <130> FILE REFERENCE: 6235-76051-01
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/584,482
C--> 11 <141> CURRENT FILING DATE: 2006-06-23
    13 <150> PRIOR APPLICATION NUMBER: JP 2003-435085
    14 <151> PRIOR FILING DATE: 2003-12-26
    16 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/019393
    17 <151> PRIOR FILING DATE: 2004-12-24
    19 <160> NUMBER OF SEQ ID NOS: 5
    21 <170> SOFTWARE: PatentIn version 3.1
    23 <210> SEQ ID NO: 1
    24 <211> LENGTH: 1965
    25 <212> TYPE: DNA
    26 <213> ORGANISM: Homo sapiens
    28 <220> FEATURE:
    29 <221> NAME/KEY: CDS
    30 <222> LOCATION: (1)..(1965)
    31 <223> OTHER INFORMATION:
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    34 atg gag cgg aaa gtg ctt gcg ctc cag gcc cga aag aaa agg acc aag    48
    35 Met Glu Arg Lys Val Leu Ala Leu Gln Ala Arg Lys Lys Arg Thr Lys
    36 1               5                   10                  15
    38 gcc aag aag gac aaa gcc caa agg aaa tct gaa act cag cac cga ggc    96
    39 Ala Lys Lys Asp Lys Ala Gln Arg Lys Ser Glu Thr Gln His Arg Gly
    40              20                  25                  30
    42 tct gct ccc cac tct gag agt gat cta cca gag cag gaa gag gag att   144
    43 Ser Ala Pro His Ser Glu Ser Asp Leu Pro Glu Gln Glu Glu Glu Ile
    44          35                  40                  45
    46 ctg gga tct gat gat gat gag caa gaa gat cct aat gat tat tgt aaa   192
    47 Leu Gly Ser Asp Asp Asp Glu Gln Glu Asp Pro Asn Asp Tyr Cys Lys
    48      50                  55                  60
    50 gga ggt tat cat ctt gtg aaa att gga gat cta ttc aat ggg aga tac   240
    51 Gly Gly Tyr His Leu Val Lys Ile Gly Asp Leu Phe Asn Gly Arg Tyr
    52 65                  70                  75                  80
    54 cat gtg atc cga aag tta ggc tgg gga cac ttt tca aca gta tgg tta   288
    55 His Val Ile Arg Lys Leu Gly Trp Gly His Phe Ser Thr Val Trp Leu
    56                  85                  90                  95
    58 tca tgg gat att cag ggg aag aaa ttt gtg gca atg aaa gta gtt aaa   336
    59 Ser Trp Asp Ile Gln Gly Lys Lys Phe Val Ala Met Lys Val Val Lys
    60                  100                 105                 110
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62 agt gct gaa cat tac act gaa aca gca cta gat gaa atc cgg ttg ctg   384

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63  Ser Ala Glu His Tyr Thr Glu Thr Ala Leu Asp Glu Ile Arg Leu Leu
64          115                 120                 125
66  aag tca gtt cgc aat tca gac cct aat gat cca aat aga gaa atg gtt    432
67  Lys Ser Val Arg Asn Ser Asp Pro Asn Asp Pro Asn Arg Glu Met Val
68          130                 135                 140
70  gtt caa cta cta gat gac ttt aaa ata tca gga gtt aat gga aca cat    480
71  Val Gln Leu Leu Asp Asp Phe Lys Ile Ser Gly Val Asn Gly Thr His
72  145                 150                 155                 160
74  atc tgc atg gta ttt gaa gtt ttg ggg cat cat ctg ctc aag tgg atc    528
75  Ile Cys Met Val Phe Glu Val Leu Gly His His Leu Leu Lys Trp Ile
76                  165                 170                 175
78  atc aaa tcc aat tat cag ggg ctt cca ctg cct tgt gtc aaa aaa att    576
79  Ile Lys Ser Asn Tyr Gln Gly Leu Pro Leu Pro Cys Val Lys Lys Ile
80                  180                 185                 190
82  att cag caa gtg tta cag ggt ctt gat tat tta cat acc aag tgc cgt    624
83  Ile Gln Gln Val Leu Gln Gly Leu Asp Tyr Leu His Thr Lys Cys Arg
84          195                 200                 205
86  atc atc cac act gac att aaa cca gag aac atc tta ttg tca gtg aat    672
87  Ile Ile His Thr Asp Ile Lys Pro Glu Asn Ile Leu Leu Ser Val Asn
88          210                 215                 220
90  gag cag tac att cgg agg ctg gct gca gaa gca aca gaa tgg cag cga    720
91  Glu Gln Tyr Ile Arg Arg Leu Ala Ala Glu Ala Thr Glu Trp Gln Arg
92  225                 230                 235                 240
94  tct gga gct cct ccg cct tcc gga tct gca gtc agt act gct ccc cag    768
95  Ser Gly Ala Pro Pro Pro Ser Gly Ser Ala Val Ser Thr Ala Pro Gln
96                  245                 250                 255
98  cct aaa cca gct gac aaa atg tca aag aat aag aag aag aaa ttg aag    816
99  Pro Lys Pro Ala Asp Lys Met Ser Lys Asn Lys Lys Lys Lys Leu Lys
100                 260                 265                 270
102 aag aag cag aag cgc cag gca gaa tta cta gag aag cga atg cag gaa    864
103 Lys Lys Gln Lys Arg Gln Ala Glu Leu Leu Glu Lys Arg Met Gln Glu
104         275                 280                 285
106 att gag gaa atg gag aaa gag tcg ggc cct ggg caa aaa aga cca aac    912
107 Ile Glu Glu Met Glu Lys Glu Ser Gly Pro Gly Gln Lys Arg Pro Asn
108         290                 295                 300
110 aag caa gaa gaa tca gag agt cct gtt gaa aga ccc ttg aaa gag aac    960
111 Lys Gln Glu Glu Ser Glu Ser Pro Val Glu Arg Pro Leu Lys Glu Asn
112 305                 310                 315                 320
114 cca cct aat aaa atg acc caa gaa aaa ctt gaa gag tca agt acc att   1008
115 Pro Pro Asn Lys Met Thr Gln Glu Lys Leu Glu Glu Ser Ser Thr Ile
116                 325                 330                 335
118 ggc cag gat caa acg ctt atg gaa cgt gat aca gag ggt ggt gca gca   1056
119 Gly Gln Asp Gln Thr Leu Met Glu Arg Asp Thr Glu Gly Gly Ala Ala
120         340                 345                 350
122 gaa att aat tgc aat gga gtg att gaa gtc att aat tat act cag aac   1104
123 Glu Ile Asn Cys Asn Gly Val Ile Glu Val Ile Asn Tyr Thr Gln Asn
124         355                 360                 365
126 agt aat aat gaa aca ttg aga cat aaa gag gat cta cat aat gct aat   1152
127 Ser Asn Asn Glu Thr Leu Arg His Lys Glu Asp Leu His Asn Ala Asn
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128     370                     375                     380
130 gac tgt gat gtc caa aat ttg aat cag gaa tct agt ttc cta agc tcc      1200
131 Asp Cys Asp Val Gln Asn Leu Asn Gln Glu Ser Ser Phe Leu Ser Ser
132 385                     390                     395                     400
134 caa aat gga gac agc agc aca tct caa gaa aca gac tct tgt aca cct      1248
135 Gln Asn Gly Asp Ser Ser Thr Ser Gln Glu Thr Asp Ser Cys Thr Pro
136                     405                     410                     415
138 ata aca tct gag gtg tca gac acc atg gtg tgc cag tct tcc tca act      1296
139 Ile Thr Ser Glu Val Ser Asp Thr Met Val Cys Gln Ser Ser Ser Thr
140                     420                     425                     430
142 gta ggt cag tca ttc agt gaa caa cac att agc caa ctt caa gaa agc      1344
143 Val Gly Gln Ser Phe Ser Glu Gln His Ile Ser Gln Leu Gln Glu Ser
144             435                     440                     445
146 att cgg gca gag ata ccc tgt gaa gat gaa caa gag caa gaa cat aac      1392
147 Ile Arg Ala Glu Ile Pro Cys Glu Asp Glu Gln Glu Gln Glu His Asn
148     450                     455                     460
150 gga cca ctg gac aac aaa gga aaa tcc acg gct gga aat ttt ctt gtt      1440
151 Gly Pro Leu Asp Asn Lys Gly Lys Ser Thr Ala Gly Asn Phe Leu Val
152 465                     470                     475                     480
154 aat ccc ctt gag cca aaa aat gca gaa aag ctc aag gtg aag att gct      1488
155 Asn Pro Leu Glu Pro Lys Asn Ala Glu Lys Leu Lys Val Lys Ile Ala
156                     485                     490                     495
158 gac ctt gga aat gct tgt tgg gtg cac aaa cat ttc act gaa gat att      1536
159 Asp Leu Gly Asn Ala Cys Trp Val His Lys His Phe Thr Glu Asp Ile
160             500                     505                     510
162 caa aca agg caa tat cgt tcc ttg gaa gtt cta atc gga tct ggc tat      1584
163 Gln Thr Arg Gln Tyr Arg Ser Leu Glu Val Leu Ile Gly Ser Gly Tyr
164     515                     520                     525
166 aat acc cct gct gac att tgg agc acg gca tgc atg gcc ttt gaa ctg      1632
167 Asn Thr Pro Ala Asp Ile Trp Ser Thr Ala Cys Met Ala Phe Glu Leu
168     530                     535                     540
170 gcc aca ggt gac tat ttg ttt gaa cct cat tca ggg gaa gag tac act      1680
171 Ala Thr Gly Asp Tyr Leu Phe Glu Pro His Ser Gly Glu Glu Tyr Thr
172 545                     550                     555                     560
174 cga gat gaa gat cac att gca ttg atc ata gaa ctt ctg ggg aag gtg      1728
175 Arg Asp Glu Asp His Ile Ala Leu Ile Ile Glu Leu Leu Gly Lys Val
176             565                     570                     575
178 cct cgc aag ctc att gtg gca gga aaa tat tcc aag gaa ttt ttc acc      1776
179 Pro Arg Lys Leu Ile Val Ala Gly Lys Tyr Ser Lys Glu Phe Phe Thr
180             580                     585                     590
182 aaa aaa ggt gac ctg aaa cat atc acg aag ctg aaa cct tgg ggc ctt      1824
183 Lys Lys Gly Asp Leu Lys His Ile Thr Lys Leu Lys Pro Trp Gly Leu
184             595                     600                     605
186 ttt gag gtt cta gtg gag aag tat gag tgg tcg cag gaa gag gca gct      1872
187 Phe Glu Val Leu Val Glu Lys Tyr Glu Trp Ser Gln Glu Glu Ala Ala
188     610                     615                     620
190 ggc ttc aca gat ttc tta ctg ccc atg ttg gag ctg atc cct gag aag      1920
191 Gly Phe Thr Asp Phe Leu Leu Pro Met Leu Glu Leu Ile Pro Glu Lys
192 625                     630                     635                     640
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194 aga gcc act gcc gcc gag tgt ctc cgg cac cct tgg ctt aac tcc          1965
195 Arg Ala Thr Ala Ala Glu Cys Leu Arg His Pro Trp Leu Asn Ser
196             645             650                 655
199 <210> SEQ ID NO: 2
200 <211> LENGTH: 655
201 <212> TYPE: PRT
202 <213> ORGANISM: Homo sapiens
204 <400> SEQUENCE: 2
205 Met Glu Arg Lys Val Leu Ala Leu Gln Ala Arg Lys Lys Arg Thr Lys
206 1               5                   10                  15
208 Ala Lys Lys Asp Lys Ala Gln Arg Lys Ser Glu Thr Gln His Arg Gly
209             20                  25                  30
211 Ser Ala Pro His Ser Glu Ser Asp Leu Pro Glu Gln Glu Glu Glu Ile
212         35                  40                  45
214 Leu Gly Ser Asp Asp Asp Glu Gln Glu Asp Pro Asn Asp Tyr Cys Lys
215     50                  55                  60
217 Gly Gly Tyr His Leu Val Lys Ile Gly Asp Leu Phe Asn Gly Arg Tyr
218 65                  70                  75                  80
220 His Val Ile Arg Lys Leu Gly Trp Gly His Phe Ser Thr Val Trp Leu
221                 85                  90                  95
223 Ser Trp Asp Ile Gln Gly Lys Lys Phe Val Ala Met Lys Val Val Lys
224                 100                 105                 110
226 Ser Ala Glu His Tyr Thr Glu Thr Ala Leu Asp Glu Ile Arg Leu Leu
227         115                 120                 125
229 Lys Ser Val Arg Asn Ser Asp Pro Asn Asp Pro Asn Arg Glu Met Val
230     130                 135                 140
232 Val Gln Leu Leu Asp Asp Phe Lys Ile Ser Gly Val Asn Gly Thr His
233 145                 150                 155                 160
235 Ile Cys Met Val Phe Glu Val Leu Gly His His Leu Leu Lys Trp Ile
236                 165                 170                 175
238 Ile Lys Ser Asn Tyr Gln Gly Leu Pro Leu Pro Cys Val Lys Lys Ile
239             180                 185                 190
241 Ile Gln Gln Val Leu Gln Gly Leu Asp Tyr Leu His Thr Lys Cys Arg
242         195                 200                 205
244 Ile Ile His Thr Asp Ile Lys Pro Glu Asn Ile Leu Leu Ser Val Asn
245     210                 215                 220
247 Glu Gln Tyr Ile Arg Arg Leu Ala Ala Glu Ala Thr Glu Trp Gln Arg
248 225                 230                 235                 240
250 Ser Gly Ala Pro Pro Pro Ser Gly Ser Ala Val Ser Thr Ala Pro Gln
251             245                 250                 255
253 Pro Lys Pro Ala Asp Lys Met Ser Lys Asn Lys Lys Lys Leu Lys
254             260                 265                 270
256 Lys Lys Gln Lys Arg Gln Ala Glu Leu Leu Glu Lys Arg Met Gln Glu
257         275                 280                 285
259 Ile Glu Glu Met Glu Lys Glu Ser Gly Pro Gly Gln Lys Arg Pro Asn
260     290                 295                 300
262 Lys Gln Glu Glu Ser Glu Ser Pro Val Glu Arg Pro Leu Lys Glu Asn
263 305                 310                 315                 320
265 Pro Pro Asn Lys Met Thr Gln Glu Lys Leu Glu Glu Ser Ser Thr Ile
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RAW SEQUENCE LISTING   DATE: 07/07/2006
PATENT APPLICATION: US/10/584,482   TIME: 14:52:51

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\07072006\J584482.raw**

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266                   325                 330                 335
268 Gly Gln Asp Gln Thr Leu Met Glu Arg Asp Thr Glu Gly Gly Ala Ala
269               340                 345                 350
271 Glu Ile Asn Cys Asn Gly Val Ile Glu Val Ile Asn Tyr Thr Gln Asn
272           355                 360                 365
274 Ser Asn Asn Glu Thr Leu Arg His Lys Glu Asp Leu His Asn Ala Asn
275       370                 375                 380
277 Asp Cys Asp Val Gln Asn Leu Asn Gln Glu Ser Ser Phe Leu Ser Ser
278 385               390                 395                 400
280 Gln Asn Gly Asp Ser Ser Thr Ser Gln Glu Thr Asp Ser Cys Thr Pro
281               405                 410                 415
283 Ile Thr Ser Glu Val Ser Asp Thr Met Val Cys Gln Ser Ser Ser Thr
284           420                 425                 430
286 Val Gly Gln Ser Phe Ser Glu Gln His Ile Ser Gln Leu Gln Glu Ser
287       435                 440                 445
289 Ile Arg Ala Glu Ile Pro Cys Glu Asp Glu Gln Glu Gln Glu His Asn
290     450                 455                 460
292 Gly Pro Leu Asp Asn Lys Gly Lys Ser Thr Ala Gly Asn Phe Leu Val
293 465               470                 475                 480
295 Asn Pro Leu Glu Pro Lys Asn Ala Glu Lys Leu Lys Val Lys Ile Ala
296               485                 490                 495
298 Asp Leu Gly Asn Ala Cys Trp Val His Lys His Phe Thr Glu Asp Ile
299           500                 505                 510
301 Gln Thr Arg Gln Tyr Arg Ser Leu Glu Val Leu Ile Gly Ser Gly Tyr
302       515                 520                 525
304 Asn Thr Pro Ala Asp Ile Trp Ser Thr Ala Cys Met Ala Phe Glu Leu
305     530                 535                 540
307 Ala Thr Gly Asp Tyr Leu Phe Glu Pro His Ser Gly Glu Glu Tyr Thr
308 545               550                 555                 560
310 Arg Asp Glu Asp His Ile Ala Leu Ile Ile Glu Leu Leu Gly Lys Val
311           565                 570                 575
313 Pro Arg Lys Leu Ile Val Ala Gly Lys Tyr Ser Lys Glu Phe Phe Thr
314           580                 585                 590
316 Lys Lys Gly Asp Leu Lys His Ile Thr Lys Leu Lys Pro Trp Gly Leu
317       595                 600                 605
319 Phe Glu Val Leu Val Glu Lys Tyr Glu Trp Ser Gln Glu Glu Ala Ala
320     610                 615                 620
322 Gly Phe Thr Asp Phe Leu Leu Pro Met Leu Glu Leu Ile Pro Glu Lys
323 625               630                 635                 640
325 Arg Ala Thr Ala Ala Glu Cys Leu Arg His Pro Trp Leu Asn Ser
326               645                 650                 655
329 <210> SEQ ID NO: 3
330 <211> LENGTH: 2058
331 <212> TYPE: DNA
332 <213> ORGANISM: Homo sapiens
334 <220> FEATURE:
335 <221> NAME/KEY: CDS
336 <222> LOCATION: (1)..(2058)
337 <223> OTHER INFORMATION:
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/07/2006
PATENT APPLICATION: US/10/584,482 TIME: 14:52:52

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\07072006\J584482.raw**

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5

VERIFICATION SUMMARY   DATE: 07/07/2006
PATENT APPLICATION: **US/10/584,482**   TIME: 14:52:52

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\07072006\J584482.raw**

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31
L:339 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:337